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Research Article

Studies on genetic variability and character association for yield and its attributes in greengram [*Vigna radiata* (L.) Wilczek]

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Abstract

An experiment was carried out to estimate the genetic parameters such as variability, heritability, genetic advance, character association and path analysis for twelve quantitative characters in 50 genotypes of green gram [*Vigna radiata* (L.) Wilczek]. The GCV for all the characters studied was less than the PCV indicating the interaction of genotype with the environment. High heritability coupled with high genetic advance as per cent of mean was observed for the number of primary branches per plant, seed yield per plant, plant height, the number of pods per plant, 100 seed weight and days to 50 per cent flowering. Character association studies revealed that the number of pods per plant, the number of clusters per plant, the number of seeds per pod, the number of primary branches per plant, plant height, days to maturity, pod length and 100 seed weight showed a positive and significant correlation with seed yield per plant. Path analysis revealed that the number of pods per plant had a high positive and direct effect on seed yield.

Keywords

Genetic variability, heritability, genetic advance, character association, path analysis.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is a short duration legume crop that belongs to the Fabaceae family. It is a self-pollinating diploid legume with the chromosome number $2n=2x=22$ (Karpechenko, 1925). Mungbean probably originated in India (De Candolle, 1886) or the Indo-Burma region (Vavilov, 1951). Mungbean occupies an important position due to its high seed protein content (22-24%) and it has the ability to restore seed fertility through symbiotic nitrogen fixation (Malik, 1994). This crop is grown in cropping systems as a mixed crop, catch crop, sequential crop besides being grown as a sole crop under residual soil moisture conditions after the harvest of rice and also, before and after the harvest of other summer crops under semi irrigated and dryland conditions. The productivity of pulse crops are very low as compared to cereals, the reason being growing of the crop in less fertile soils with minimum inputs and unavailability of cultivars with high yield potential adapted to local conditions.

Yield is a complex trait governed by the interaction of many variables hence, the selection simply based on yield is not effective. The efficiency of selection would increase if the nature and magnitude of interrelationship among component characters and seed yield is well understood. Knowledge of heritability and genetic advance of the character indicate the scope for improvement of a trait through selection. Heritability estimates along with genetic advances are also helpful in predicting the genetic gain under selection. Correlation coefficient analysis elaborates the degree and extent of the relationship among important plant characters and it provides basic criteria for selection and leads to the directional model based on yield and its components in the field experiments but the information it supplies about nature of the association is often incomplete. Path coefficient analysis is an efficient statistical technique, specially designed to quantify the interrelationship of different components and their direct

and indirect effects on seed yield. Through this technique, yield attributing characters can be ranked and the specific traits, producing a given correlation can be headed (Rao *et al.*, 2006). The objective of the present study was to determine the variability parameters along with the correlation and path analysis is to understand the mode of inheritance and degree and direction of association of different yield component traits with the seed yield.

MATERIAL AND METHODS

The present investigation was carried out during Rabi, 2018 at dryland farm of Regional Agricultural Research Station, Tirupati. The experimental material comprised of 50 green gram genotypes, which were raised in Randomised Block Design with three replications. Each genotype was sown in three rows of 4 m length with a spacing of 30 cm X 10 cm. Twelve traits *viz.*, plant height (cm), days to 50 per cent flowering, days to maturity, the number of primary branches per plant, the number of clusters per plant, the number of pods per plant, pod length (cm), the number of seeds per pod, harvest index (%), hundred seed weight (gm), Soil Plant Analysis Development (SPAD) chlorophyll meter reading and seed yield per plant (gm) were recorded from randomly selected plants in each of the genotypes per replication, except days to 50 per cent flowering and

days to maturity which were recorded on plot basis. The statistical analysis for variance was worked out according to Panse and Sukhatme (1961). Phenotypic and genotypic coefficients of variation were calculated based on the method advocated by Burton (1952). Heritability, genetic advance as per cent of mean and correlation coefficients were estimated as per the formula given by Johnson *et al.* (1955). The path coefficient analysis was worked as suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters studied, which gives the evidence of sufficient variability among the genotypes. The estimates of the phenotypic coefficients of variation were higher than the genotypic coefficient of variation indicating the influence of the environment in governing the characters.

Maximum estimate of phenotypic coefficient of variation was recorded for the number of branches per plant (90.73 %) followed by seed yield per plant (31.69 %), the number of pods per plant (29.55 %), plant height (25.98 %) and the number of clusters per plant (24.30 %) indicating the presence of sufficient phenotypic variability for these traits.

Table 1. Range, mean, coefficient of variation, heritability (broad sense) and genetic advance as percent of the mean for yield attributes in green gram

S. No	Characters	Mean	Range		Variance		Coefficient of variation		Heritability (Broad sense)	Genetic advance (GA)	GA as percent of mean (%)
			Min	Max	Geno- typic	Pheno- typic	Geno- typic (%)	Pheno- typic (%)			
1	Plant height (cm)	27.92	14.29	43.63	43.76	52.62	23.70	25.98	83.17	12.43	44.52
2	Days to 50% flowering	33.49	27.33	41.33	15.19	15.81	11.63	11.87	96.08	7.87	23.50
3	Days to maturity	68.89	60.00	74.33	9.30	9.99	4.43	4.59	93.05	6.06	8.80
4	No. of branches per plant	0.64	0.00	2.27	0.32	0.33	89.24	90.73	96.75	1.15	180.83
5	No. of clusters per plant	5.91	2.93	8.07	0.96	2.02	16.60	24.30	47.43	1.39	23.54
6	Pod length (cm)	6.93	6.05	9.26	0.43	0.52	9.49	10.43	82.80	1.23	17.79
7	No. of seeds per pod	9.75	7.13	12.60	0.98	1.56	10.16	12.82	62.84	1.62	16.59
8	No. of pods per plant	14.03	6.33	25.20	13.35	18.08	25.39	29.55	73.83	6.47	44.94
9	Harvest index (%)	34.04	18.92	41.28	10.10	24.07	9.34	14.42	41.95	4.24	12.46
10	100 seed weight (g)	3.76	3.00	5.33	0.38	0.44	16.33	17.67	85.51	1.17	31.12
11	SCMR	44.34	40.33	46.37	1.43	1.96	2.70	3.16	72.99	2.11	4.75
12	Seed yield per plant (g)	4.68	2.40	9.30	1.64	2.20	27.37	31.69	74.59	2.28	48.69

Low estimates of the phenotypic coefficient of variation were recorded for SPAD chlorophyll meter reading (3.16 %) and days to maturity (4.59 %). Characterization of range of variation was done as proposed by Sivasubramanian and Madhava Menon (1973). These results are in accordance with Kate *et al.* (2017) and Degefa *et al.* (2014) for the number of primary branches per plant; Garg *et al.* (2017) and Jagdhane *et al.* (2017) for the number of pods per plant; Rasal and Parhe, (2017) and Yadav *et al.* (2017) for

seed yield per plant; Baisakh *et al.* (2016) and Sunayana *et al.* (2017) for plant height; Payasi (2015) for the number of clusters per plant; Makeen *et al.* (2007) and Sunayana *et al.* (2017) for days to maturity and Paramesh *et al.* (2014) for SPAD chlorophyll meter reading.

Quantitative characters are influenced more by the environment, obstructing the transmission of the phenotype observed to the next generation. Therefore,

the study on the heritable portion of the variability is necessary. Heritability is a good index of characters from parents to offsprings and helps as a tool for the selection of elite genotypes. Heritability estimates are categorized by Johnson *et al.* (1955). In the present study, highest heritability was recorded for the number of primary branches per plant (96.75 %) followed by days to 50 % flowering (96.08 %), days to maturity (93.05%), 100 seed weight (85.51 %), plant height (83.17 %), pod length (82.80 %), seed yield per plant (74.59 %), the number of pods per plant (73.83 %), SPAD chlorophyll meter reading (72.99 %) and the number of seeds per pod (62.84 %).

High heritability alone is not enough to exercise the selection unless the information is accompanied by a substantial amount of genetic advance. High heritability coupled with high genetic advance as per cent of mean was recorded for the number of primary branches per plant, seed yield per plant, plant height, the number of pods per plant, 100 seed weight and days to 50 % flowering. This suggests that most likely the heritability is due to additive gene effects and hence the selection may be effective for these characters. It may be suggested that for additive effects pedigree or modified pedigree method of selection is followed. Similar findings were obtained by Choudary

et al. (2017) for the number of primary branches per plant; Ghimire *et al.* (2017) for seed yield per plant; Makeen *et al.* (2007) for plant height; Rahim *et al.* (2010) for the number of pods per plant; Kumar *et al.* (2013) for 100 seed weight and Payasi (2015) for days to 50% flowering.

Genotypic correlations were higher than the phenotypic correlations (Table 2) for most of the characters, which can be explained due to the masking or modifying effects of the environment on the genetic association between characters. In the present investigation, seed yield per plant recorded high significant and positive association with the number of pods per plant ($r_p = 0.810^{**}$ and $r_g = 0.834^{**}$), followed by the number of clusters per plant ($r_p = 0.440^{**}$ and $r_g = 0.534^{**}$), the number of seeds per pod ($r_p = 0.390^{**}$ and $r_g = 0.530^{**}$), the number of primary branches per plant ($r_p = 0.396^{**}$ and $r_g = 0.472^{**}$), plant height ($r_p = 0.392^{**}$ and $r_g = 0.465^{**}$), days to maturity ($r_p = 0.320^{**}$ and $r_g = 0.355^{**}$), pod length ($r_p = 0.212^{**}$ and $r_g = 0.252^{**}$) and 100 seed weight ($r_p = 0.172^{**}$ and $r_g = 0.224^{**}$). These results are in accordance with Ramakrishnan *et al.* (2018) for the number of pods per plant; Sandhiya and Saravanan (2018) for the number of clusters per plant; Das and Barua (2015) for the number of seeds per pod; Ghimire *et al.* (2017) for the number of primary branches

Table 2. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among twelve yield attributing characters in greengram

Characters		Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pod length (cm)	Seeds per pod	Pods per plant	Harvest index (%)	100 seed weight (g)	SCMR	Seed yield per plant (g)
Plant height (cm)	r_p	0.643**	0.564**	0.052	0.240**	0.161*	0.547**	0.382**	-0.195*	-0.396**	-0.196*	0.392**
	r_g	0.724**	0.638**	0.045	0.293**	0.188*	0.707**	0.450**	-0.394**	-0.431**	-0.277**	0.465**
Days to 50 % flowering	r_p		0.458**	-0.038	-0.064	0.044	0.280**	0.105	-0.365**	-0.231**	0.014	0.110
	r_g		0.479**	-0.044	-0.078	0.032	0.318**	0.154	-0.535**	-0.267**	0.006	0.152
Days to maturity	r_p			0.011	0.349**	0.057	0.358**	0.454**	-0.162*	-0.330**	-0.318**	0.320**
	r_g			0.006	0.506**	0.049	0.458**	0.525**	-0.298**	-0.393**	-0.376**	0.355**
Branches per Plant	r_p				0.427**	-0.151	0.057	0.453**	0.029	-0.199*	-0.052	0.396**
	r_g				0.589**	-0.187*	0.035	0.532**	0.046	-0.220**	-0.060	0.472**
Clusters per plant	r_p					-0.087	0.172*	0.614**	0.156	-0.299**	-0.181*	0.440**
	r_g					-0.193*	0.116	0.760**	0.074	-0.476**	-0.252**	0.534**
Pod length (cm)	r_p						0.474**	-0.042	-0.168*	0.295**	-0.076	0.212**
	r_g						0.438**	-0.055	-0.225**	0.352**	-0.125	0.252**
Seeds per pod	r_p							0.375**	-0.171*	-0.368**	-0.301**	0.390**
	r_g							0.500**	-0.329**	-0.455**	-0.390**	0.530**
Pods per plant	r_p								0.108	-0.446**	-0.282**	0.810**
	r_g								-0.103	-0.554**	-0.351**	0.834**
Harvest index (%)	r_p									0.053	0.079	0.109
	r_g									0.086	0.189*	-0.120
100 seed weight (g)	r_p										0.184*	0.172*
	r_g										0.220**	0.224**
SCMR	r_p											-0.345**
	r_g											-0.450**

*,** Significant at 5% and 1% level , respectively

per plant; Baisakh *et al.* (2016) for plant height; Kate *et al.* (2017) for days to maturity; Jyothsna *et al.* (2016) for pod length and Kate *et al.* (2017) for 100 seed weight. Hence, these characters can be utilized in indirect selection so as to improve the seed yield per plant.

Table 3. Direct and indirect effects of yield component characters on seed yield in greengram

Characters		Plant height (cm)	Days to 50% flowering	Days to maturity	Branches per plant	Clusters per plant	Pod length (cm)	Seeds per pod	Pods per plant	Harvest index (%)	100 seed weight (g)	SCMR	Seed yield per plant (g)
Plant height (cm)	P	0.177	0.029	-0.075	0.005	-0.020	0.316	-0.023	0.330	-0.016	-0.077	-0.031	0.392**
	G	0.704	-0.273	-0.014	0.011	-0.193	0.062	-0.400	0.556	-0.012	-0.025	-0.049	0.465**
Days to 50 % flowering	P	0.114	0.046	-0.061	-0.004	-0.005	0.009	-0.012	0.091	-0.031	-0.045	-0.002	0.110
	G	0.510	-0.377	-0.011	-0.010	0.051	0.011	-0.178	0.190	-0.017	-0.015	-0.001	0.152
Days to maturity	P	0.099	0.021	-0.134	0.001	-0.029	0.011	-0.015	0.392	-0.014	-0.064	0.051	0.320**
	G	0.449	-0.181	-0.022	-0.001	-0.334	0.016	-0.259	0.649	-0.009	-0.022	0.067	0.355**
Branches per plant	P	0.009	-0.002	-0.002	0.095	-0.034	-0.030	-0.002	0.391	0.003	-0.039	0.008	0.396**
	G	0.032	0.017	-0.0001	0.237	-0.389	-0.062	-0.020	0.658	0.001	-0.013	0.011	0.472**
Clusters per plant	P	0.042	-0.003	-0.047	-0.040	-0.083	-0.017	-0.007	0.530	0.013	-0.058	0.029	0.440**
	G	0.206	0.029	-0.001	0.140	-0.660	-0.064	-0.066	0.940	0.002	-0.271	0.045	0.534**
Pod length (cm)	P	0.028	0.002	-0.008	-0.014	0.007	0.197	-0.020	-0.036	-0.014	0.057	0.012	0.212**
	G	0.133	-0.012	-0.001	-0.044	0.127	0.330	-0.248	-0.068	-0.007	0.020	0.022	0.252**
Seeds per pod	P	0.200	0.013	-0.048	0.005	-0.014	0.093	-0.042	0.324	-0.014	-0.072	0.048	0.390**
	G	0.500	-0.118	-0.010	0.008	-0.077	0.145	-0.566	0.618	-0.010	-0.026	0.069	0.530**
Pods per plant	P	0.068	0.004	-0.061	0.043	-0.051	-0.008	-0.016	0.864	0.009	-0.087	0.045	0.810**
	G	0.317	-0.058	-0.012	0.126	-0.502	-0.018	-0.283	1.236	-0.003	-0.032	0.062	0.834**
Harvest index (%)	P	-0.035	-0.017	0.022	0.003	-0.013	-0.033	0.007	0.093	0.084	0.010	-0.013	0.109
	G	-0.277	0.202	0.007	0.011	-0.049	-0.074	0.186	-0.127	0.031	0.005	-0.033	-0.120
100 seed weight (g)	P	-0.077	-0.011	0.044	-0.019	0.025	0.058	0.015	-0.384	0.004	0.195	-0.029	0.172*
	G	-0.304	0.100	0.009	-0.052	0.314	0.116	0.257	-0.685	0.003	0.057	-0.039	0.224**
SCMR	P	-0.035	0.001	0.042	-0.005	0.015	-0.015	0.013	-0.244	-0.007	0.036	-0.160	-0.345**
	G	-0.195	-0.002	0.008	-0.014	0.166	-0.041	0.221	-0.435	0.006	0.013	-0.177	-0.450**

*, ** Significant at 5% and 1% level, respectively. Residual effect: Phenotypic = 0.460, Genotypic = 0.317

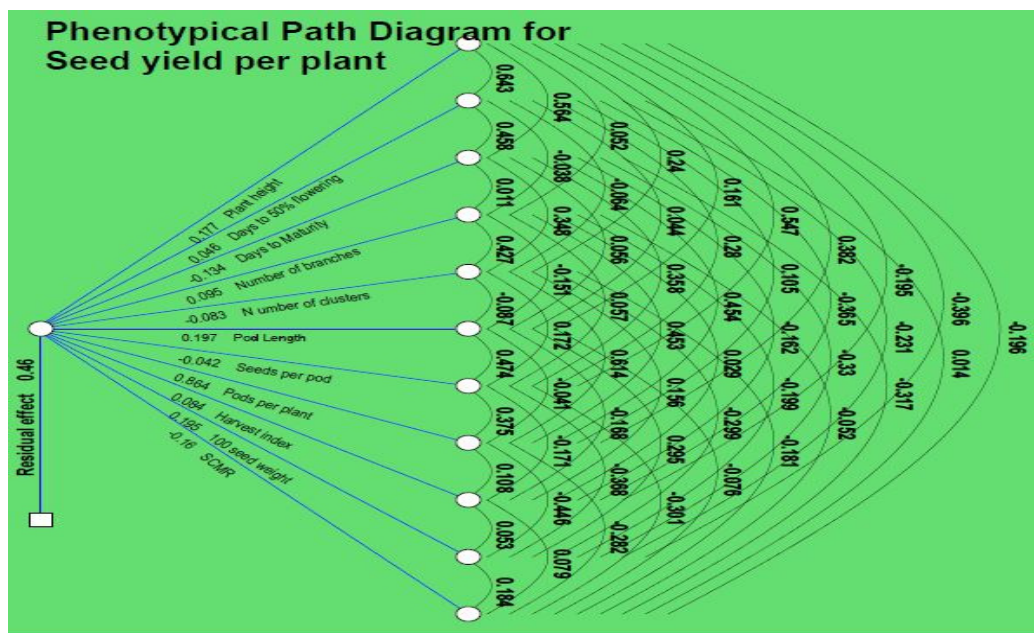


Fig 1. Phenotypic path diagram of seed yield and yield components in green gram

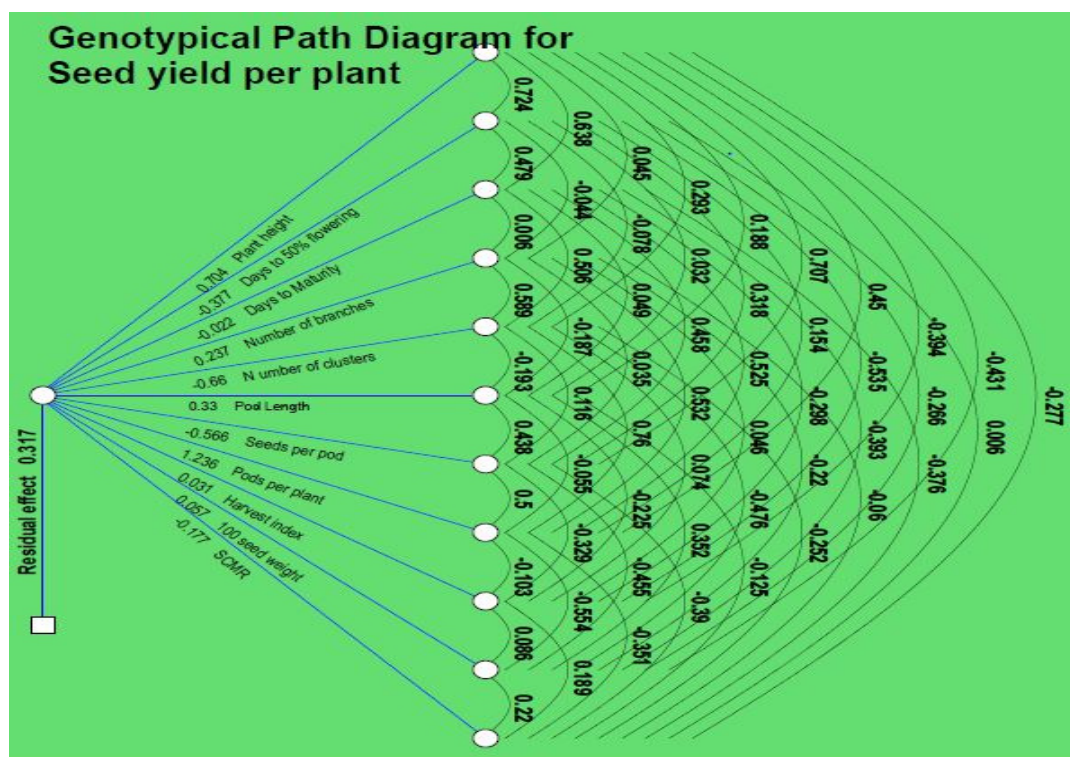


Fig 2. Genotypic path diagram of seed yield and yield components in green gram

Path coefficient analysis revealed that the number of pods per plant had a positive and direct effect on seed yield per plant ($P = 0.864$ and $G = 1.236$) followed by pod length ($P = 0.197$ and $G = 0.330$), 100 seed weight ($P = 0.195$ and $G = 0.057$), plant height ($P = 0.177$ and $G = 0.704$), the number of primary branches per plant ($P = 0.095$ and $G = 0.237$), harvest index ($P = 0.084$ and $G = 0.031$) and days to 50% flowering ($P = 0.046$ and $G = -0.377$). (Table 3, Fig 1 and Fig 2) showed a true relationship with seed yield per plant by plant establishing significant and positive direct effects both at the genotypic and phenotypic levels. Similar findings were obtained by Ramakrishnan *et al.* (2018) for the number of pods per plant and plant height; Thippani *et al.* (2013) for pod length and 100 seed weight; Kate *et al.* (2017) for the number of primary branches per plant; Garg *et al.* (2017) for harvest index and days to 50% flowering. The residual effect was 0.460, indicating that along with the present characters there are some more characters like pods per cluster, biological yield per plant, pod yield per plant should be taken into consideration while formulating selection strategies for the yield improvement.

The present investigation registered a high heritability along with high the genetic advance as per cent of mean for the number of primary branches per plant, seed yield per plant, plant height, the number of pods per plant, 100 seed weight and days to 50% flowering suggesting that these characters should be given top priority while exercising the selection. Considering the nature and magnitude of

character association and their direct and indirect effects it can be concluded that the improvement in seed yield is possible through the simultaneous manifestation of pods per plant, the number of primary branches per plant, pod length, plant height, and 100-seed weight.

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